**Pending Claims**

1. A method of labeling individual mammalian chromosomes in interphase cells by *in situ* hybridization, comprising:

providing chromosome-specific labeled probes and competitor DNA;

combining the labeled probes and competitor DNA with mammalian chromosomes in interphase cells under hybridization conditions wherein the labeled probes hybridize specifically to the mammalian chromosomes, thereby labeling the mammalian chromosomes in interphase cells, wherein the labeled probes and the competitor DNA are DNA fragments are smaller than 500 nucleotides in length.

4. The method of claim 1, wherein the labeled probes are selected from the group consisting of probes comprising total recombinant library DNA, probes comprising DNA inserts purified from a chromosome-derived recombinant DNA library, and probes comprising specific DNA fragments derived from chromosomes.

5. The method of claim 4, wherein the labeled probes are selected from the group consisting of probes labeled with at least one fluorochrome, probes labeled with at least one member of a specific binding pair, and probes labeled with an enzyme.

6. The method of claim 5, wherein the fluorochrome is selected from the group consisting of fluorescein, rhodamine, Texas red, Lucifer yellow, phycobiliproteins and cyanin dyes.

7. A method of assessing chromosomal aberrations in human interphase cells by chromosomal *in situ* suppression hybridization, comprising:

providing labeled probes specific for human chromosomal aberrations and competitor DNA;

combining the labeled probes and competitor DNA with human chromosomes in interphase cells under hybridization conditions wherein the labeled probes hybridize specifically to the human chromosomes; and

detecting the labeled probes in order to assess chromosomal aberrations in human chromosomes in interphase cells.

16. A method of determining over-representation or under-representation of a selected chromosome or a portion thereof in human tumor interphase cells comprising the steps of:

selecting a chromosome or portion thereof;

treating the human tumor interphase cells to render nucleic acid sequences present in the cells available for hybridization;

combining the human tumor interphase cells with a hybridization mixture comprising labeled DNA fragments derived from the selected chromosome, competitor DNA, and nonhuman genomic DNA, under conditions appropriate for hybridization of complementary nucleic acid sequences to occur; and

detecting labeled DNA fragments derived from the selected chromosome in order to determine the over-representation or under-representation of the selected chromosome or a portion thereof in human tumor interphase cells.